Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 10, at the end of the application.

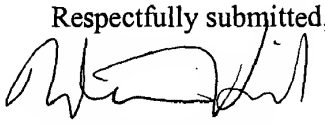
REMARKS

Applicants request entry of this amendment in adherence with 37 C.F.R. §§1.821 to 1.825. This amendment is accompanied by a floppy disk containing the above named sequences, SEQ ID NOS:1-9, in computer readable form, and a paper copy of the sequence information which has been printed from the floppy disk.

The information contained in the computer readable disk was prepared through the use of the software program "PatentIn" and is identical to that of the paper copy. This amendment contains no new matter.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 415-576-0200.

Respectfully submitted,



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VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification:

Paragraph beginning at line 20 of page 9 has been amended as follows:

A "promoter from a *IND1* gene" or "*IND1* promoter" will typically be about 500 to about 3000 nucleotides in length, usually from about 750 to 2750. Exemplary promoter sequences are shown as SEQ ID NO:3 and SEQ ID NO:4. SEQ ID NO:3 represents the 5' untranslated region of the *IND1* and SEQ ID NO:4 ~~SEQ ID NO:3~~ represents the 3' untranslated region of *IND1*. A IND1 promoter can also be identified by its ability to direct expression in the valve margin of fruit. In particular, the Ind1 promoeter directs expression at the valve margin of developing gynoecium just prior to fertilization (stage 13) through the maturation of the fruit (stage 17). The promoter does not provide significant expression in leaf tissue.

Paragraph beginning at line 29 of page 9 has been amended as follows:

An "IND1 polypeptide" is a sequence of about 50 to about 200, sometimes 100 to 190, and preferably 198 amino acid residues encoded by a IND1 polynucleotide. IND1 polypeptides are characterized by the presence of an basic helix-loop-helix (HLH) domain which bind specific polynucleotide sequences. For instance amino acid residues ISDDPQTVVARRRRERISEKIRILKRIVPGGAKMDTASMLDEAIRYTKFLK (SEQ ID NO:7) represent the HLH domain of the polypeptide shown in SEQ ID NO:2. The HLH domain is known in the art and is shared by other transcription factors including uncharacterized sequences represented by GenBank accession number E1283552 and 2262147 and the gene product, PIF3 (Ni *et al. Cell* 95:657 (1998)). The HLH domain of IND1 is therefore a DNA binding domain.

Paragraph beginning at line 1 of page 15 has been amended as follows:

Appropriate primers and probes for identifying genes such as *IND1* from plant tissues are generated from comparisons of the sequences provided herein. For a general overview of PCR

see PCR Protocols: A Guide to Methods and Applications. (Innis, M, Gelfand, D., Sninsky, J. and White, T., eds.), Academic Press, San Diego (1990). Appropriate primers for amplification of the genomic region of *IND1* or the *IND1* cDNA include the following primer pairs: 5'-gatgaaaatggaaaatggtatgtata-3' (SEQ ID NO:8) and 5'-gttcatcagggttgggagttgtg-3' (SEQ ID NO:9). The amplification conditions are typically as follows. Reaction components: 10 mM Tris-HCl, pH 8.3, 50 mM potassium chloride, 1.5 mM magnesium chloride, 0.001% gelatin, 200 μM dATP, 200 μM dCTP, 200 μM dGTP, 200 μM dTTP, 0.4 μM primers, and 100 units per ml Taq polymerase. Program: 96 C for 3 min., 30 cycles of 96 C for 45 sec., 50 C for 60 sec., 72 for 60 sec, followed by 72 C for 5 min.